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1600

1647 #13

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/668,314B

DATE: 06/21/2002

TIME: 14:06:57

Input Set : A:\6280NCP.txt

Output Set: N:\CRF3\06212002\I668314B.raw

5 <110> APPLICANT: Gurney, et al

8 <120> TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
USES

9 THEREOF

12 <130> FILE REFERENCE: 28341/6280NCP

15 <140> CURRENT APPLICATION NUMBER: US 09/668,314B

C--> 16 <141> CURRENT FILING DATE: 2002-06-11

19 <150> PRIOR APPLICATION NUMBER: US 60/169,232

20 <151> PRIOR FILING DATE: 1999-12-06

23 <150> PRIOR APPLICATION NUMBER: US 09/416,901

24 <151> PRIOR FILING DATE: 1999-10-13

27 <150> PRIOR APPLICATION NUMBER: US 60/155,493

28 <151> PRIOR FILING DATE: 1999-09-23

31 <150> PRIOR APPLICATION NUMBER: US 09/404,133

32 <151> PRIOR FILING DATE: 1999-09-23

35 <150> PRIOR APPLICATION NUMBER: PCT/US99/20881

36 <151> PRIOR FILING DATE: 1999-09-23

39 <150> PRIOR APPLICATION NUMBER: US 60/101,594

40 <151> PRIOR FILING DATE: 1998-09-24

43 <160> NUMBER OF SEQ ID NOS: 83

46 <170> SOFTWARE: PatentIn version 3.1

49 <210> SEQ ID NO: 1

50 <211> LENGTH: 1804

51 <212> TYPE: DNA

52 <213> ORGANISM: Homo sapiens

54 <400> SEQUENCE: 1

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57	gcccc	ggagc	tggcccc	gcgc	gccctt	caag	ctgcccc	ctcc	gggtgg	ccgc	ggccacgaac	120
59	cgcgta	gttg	cgcccc	acccc	gggacc	ccgg	accctg	ccg	agcgcc	acgc	cgacggcttg	180
61	gcgctc	gccc	tggagc	ctgc	cctggc	gtcc	cccgcg	ggcg	ccgcca	aactt	cttggccatg	240
63	gtagaca	aacc	tgcagg	ggga	ctctgg	ccgc	ggctact	acc	tggaga	tgt	gatcgggacc	300
65	ccccgc	caga	agctaca	gat	tctcgt	tgac	actgga	agca	gtaact	tttg	cgtggcagga	360
67	accgcg	cact	cctacata	ga	cagtact	ttt	gacacaga	ga	ggtctag	cac	ataccgctcc	420
69	aagggt	ctttg	acgtcac	agt	gaagta	caca	caagga	agct	ggacgg	gctt	cgttggggaa	480
71	gacctc	gtca	ccatcccc	aa	aggctt	caat	acttct	tttc	ttgtca	aacat	tgccactatt	540
73	tttgaat	cgag	agaattt	ctt	tttgct	ggg	attaaat	gga	atggaat	act	tggcctagct	600
75	tatgcc	acac	ttgcca	agcc	atcaagt	tct	ctggag	acct	tcttcg	actc	cctggtgaca	660
77	caagcaa	aaca	tcccc	aacgt	tttctc	catg	cagatgt	gtg	gagccg	gctt	gcccgttgct	720
79	ggatct	ggga	ccaacg	gagg	tagtct	tgtc	ttgggt	ggaa	ttgaac	caag	tttgataaa	780
81	ggagaca	tct	ggtata	cccc	tatta	aggaa	gagtgg	tact	accaga	taga	aattctgaaa	840
83	ttggaa	aattg	gaggcca	aaag	cctta	aatctg	gactgc	agag	agtata	acgc	agacaaggcc	900
85	atcgtg	gaca	gtggc	accac	gctgct	gcgc	ctgcccc	caga	aggtgt	tttg	tgcggtggtg	960
87	gaagct	gttg	cccgcg	catc	tctgatt	cca	gaattct	ctg	atggtt	ttctg	gactgggtcc	1020
89	cagctg	gcgt	gctgg	acga	ttcgga	aaaca	ccttggt	ctt	acttc	cctaa	aatctccatc	1080

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91 tacctgagag atgagaactc cagcaggtca ttccgtatca caatcctgcc tcagctttac 1140
93 attcagccca tgatgggggc cggcctgaat tatgaatggt accgattcgg catttcccca 1200
95 tccacaaatg cgctgggtgat cggtgccacg gtgatggagg gcttctacgt catcttcgac 1260
97 agagcccaga agaggggtggg cttcgcagcg agcccctgtg cagaaattgc aggtgctgca 1320
99 gtgtctgaaa ttcccgggcc ttctcaaca gaggatgtag ccagcaactg tgtccccgct 1380
101 cagtctttga gcgagcccat ttgtggatt gtgtcctatg cgctcatgag cgtctgtgga 1440
103 gccatcctcc ttgtcttaat cgtcctgctg ctgctgccgt tccgggtgtca gcgtcgcccc 1500
105 cgtgaccctg aggtcgtcaa tgatgagtc tctctgggtca gacatcgctg gaaatgaata 1560
107 gccaggcctg acctcaagca accatgaact cagctattaa gaaaatcaca ttccaggggc 1620
109 agcagccggg atcgatggtg gcgctttctc ctgtgccac ccgtcttcaa tctctgttct 1680
111 gctcccagat gccttctaga ttactgtct tttgattctt gattttcaag ctttcaaate 1740
113 ctccctactt ccaagaaaaa taattaaaaa aaaaacttca ttctaaacca aaaaaaaaaa 1800
115 aaaa 1804
118 <210> SEQ ID NO: 2
119 <211> LENGTH: 518
120 <212> TYPE: PRT
121 <213> ORGANISM: Homo sapiens
123 <400> SEQUENCE: 2
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126 1 5 10 15
129 Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
130 20 25 30
133 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
134 35 40 45
137 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
138 50 55 60
141 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
142 65 70 75 80
145 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
146 85 90 95
149 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
150 100 105 110
153 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
154 115 120 125
157 Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
158 130 135 140
161 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
162 145 150 155 160
165 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
166 165 170 175
169 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
170 180 185 190
173 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
174 195 200 205
177 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
178 210 215 220
181 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
182 225 230 235 240
185 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro

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186          245          250          255
189 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
190          260          265          270
193 Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
194          275          280          285
197 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
198          290          295          300
201 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
202 305          310          315          320
205 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
206          325          330          335
209 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
210          340          345          350
213 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
214          355          360          365
217 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
218          370          375          380
221 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
222 385          390          395          400
225 Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
226          405          410          415
229 Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
230          420          425          430
233 Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
234          435          440          445
237 Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
238          450          455          460
241 Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
242 465          470          475          480
245 Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
246          485          490          495
249 Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
250          500          505          510
253 Val Arg His Arg Trp Lys
254          515
257 <210> SEQ ID NO: 3
258 <211> LENGTH: 2070
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
262 <400> SEQUENCE: 3
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265 ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc ccccctgggg      120
267 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt      180
269 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc      240
271 gtgggcagcc cccgcagac gctcaacatc ctggtggata caggcagcag taactttgca      300
273 gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca      360
275 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag      420
277 ctgggcaccg acctggtgtaag catcccccat ggccccaacg tcaactgtgcg tgccaacatt      480
279 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacacct      540

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281 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
283 ctggtaaagc agaccacagt tcccaacctc ttctccctgc agctttgtgg tgcctggcttc 660
285 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 720
287 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcgagg gtggtattat 780
289 gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
291 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
293 gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
295 ggtttctggc taggagagca gctgggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
297 ttcccagtc tctcactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1080
299 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
301 tacaagtttg ccatctcaca gtcattccac ggcactgtta tgggagctgt tatcatggag 1200
303 ggcttctacg ttgtctttga tcggggcccga aaacgaattg gctttgctgt cagcgcttgc 1260
305 catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320
307 gaagactgtg gctacaacat tccacagaca gatgagtcaa ccctcatgac catagcctat 1380
309 gtcattggct ccatctgcgc cctcttcatg ctgccactct gcctcatggt gtgtcagtgg 1440
311 cgctgcctcc gctgcctgcg ccagcagcat gatgactttg ctgatgacat ctccctgctg 1500
313 aagtgaggag gcccatgggc agaagataga gattccctg gaccacacct ccgtgggttca 1560
315 ctttggtcac aagtaggaga cacagatggc acctgtggcc agagcacctc aggaccctcc 1620
317 ccaccacca aatgcctctg ccttgatgga gaaggaaaag gctggcaagg tgggttccag 1680
319 ggactgtacc ttaggaaac agaaaagaga agaaagaagc actctgctgg cggaataact 1740
321 cttggtcacc tcaaatttaa gtcgggaaat tctgctgctt gaaacttcag ccctgaacct 1800
323 ttgtccacca ttcttttaa ttctccaacc caaagtattc ttcttttctt agtttcagaa 1860
325 gtactggcat cacacgcagg ttacctggc gtgtgtccct gtggtaccct ggcagagaag 1920
327 agaccaagct tgtttccctg ctggccaaag tcagtaggag aggatgcaca gtttgctatt 1980
329 tgcttttagag acagggactg tataaacaag cctaacattg gtgcaaagat tgcctcttga 2040
331 attaaaaaaa aaaaaaaaaa aaaaaaaaaa 2070

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334 <210> SEQ ID NO: 4

335 <211> LENGTH: 501

336 <212> TYPE: PRT

337 <213> ORGANISM: Homo sapiens

339 <400> SEQUENCE: 4

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342 1 5 10 15
345 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
346 20 25 30
349 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
350 35 40 45
353 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
354 50 55 60
357 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
358 65 70 75 80
361 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
362 85 90 95
365 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
366 100 105 110
369 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
370 115 120 125
373 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
374 130 135 140

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377 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
378 145                      150                      155                      160
381 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
382                      165                      170                      175
385 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
386                      180                      185                      190
389 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
390                      195                      200                      205
393 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
394                      210                      215                      220
397 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
398 225                      230                      235                      240
401 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
402                      245                      250                      255
405 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
406                      260                      265                      270
409 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
410                      275                      280                      285
413 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
414                      290                      295                      300
417 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
418 305                      310                      315                      320
421 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
422                      325                      330                      335
425 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
426                      340                      345                      350
429 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
430                      355                      360                      365
433 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
434                      370                      375                      380
437 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
438 385                      390                      395                      400
441 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
442                      405                      410                      415
445 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
446                      420                      425                      430
449 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
450                      435                      440                      445
453 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
454                      450                      455                      460
457 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
458 465                      470                      475                      480
461 Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
462                      485                      490                      495
465 Ile Ser Leu Leu Lys
466                      500
469 <210> SEQ ID NO: 5
470 <211> LENGTH: 1977
471 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/668,314B

DATE: 06/21/2002
TIME: 14:06:58

Input Set : A:\6280NCP.txt
Output Set: N:\CRF3\06212002\I668314B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:83; Xaa Pos. 1,2,3,4

VERIFICATION SUMMARY

DATE: 06/21/2002

PATENT APPLICATION: US/09/668,314B

TIME: 14:06:58

Input Set : A:\6280NCP.txt

Output Set: N:\CRF3\06212002\I668314B.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:5842 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0